RAW SEQUENCE LISTING
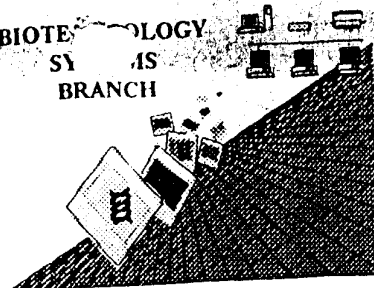# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _08/939,905 A_

Source: _1631_

Date Processed by STIC: _2-9-01_

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MAR 0 1 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212,

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO) Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

1631

RAW SEQUENCE LISTING

US/08/939,905A

A:\Sequence Listing.txt
H:\CRF3\02092001\H939905A.raw

SEQUENCE LISTING

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(v) COMPUTER READABLE FORM:

C--> 12

E.P.O format
not valid with
US applications
See correct format below

(A) APPLICATION NUMBER: US/08/939,905A

C--> 19

(B) FILING DATE: 29-Sep-1997

C--> 20

(vii) PRIOR APPLICATION DATA:

ERRORED SEQUENCES

Number of bases
differ!
- 20 listed

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: base pairs

(1) GENERAL INFORMATION:
  (i) APPLICANT:
  (ii) TITLE OF INVENTION:
  (iii) NUMBER OF SEQUENCES:
  (iv) CORRESPONDENCE ADDRESS:
     (A) ADDRESSEE:
     (B) STREET:
     (C) CITY:
     (D) STATE:
     (E) COUNTRY:
     (F) ZIP:
  (v) COMPUTER READABLE FORM:
     (A) MEDIUM TYPE:
     (B) COMPUTER:
     (C) OPERATING SYSTEM:
     (D) SOFTWARE:
  (vi) CURRENT APPLICATION DATA :
     (A) APPLICATION NUMBER:
     (B) FILING DATE:
     (C) CLASSIFICATION:
  (vii) PRIOR APPLICATION DATA
  (A) APPLICATION NUMBER:
     (B) FILING DATE:
  (viii) ATTORNEY/AGENT INFORMATION :
     (A) NAME:
     (B) REGISTRATION NUMBER:
     (C) REFERENCE/DOCKET NUMBER:
  (ix) TELECOMMUNICATION INFORMATION:
     (A) TELEPHONE:
     (B) TELEFAX:
     (C) TELEX:

17
20

W--> 452   (ii) MOLECULE TYPE: DNA

E--> 466 CTTCCAAATA TCAACTCAAT

W--> 812   (ii) MOLECULE TYPE: prt

E--> 825 NIGVLTGDEG EIRLQCNFVN GDSFGLASVA SKDAKQFLVA QSK   285

Computer program did not recognize
amino acids in single letter form possibly
due to the amino acids being in groups
of ten such as nucleic acids should be
Try three letter amino codes, 16 per line.
This occurs in sequences 15, 16, 17, 18, 19.

2901

file: C: CRF3 Outhold VsrH939905A.htm

RAW SEQUENCE LISTING

US/08/939,905A

A:\Sequence Listing.txt

N:\CRF3\02092001\H939905A.raw

W--> 856   (ii) MOLECULE TYPE: PRT

E-- > 853 SFRAAMIKMG NIGVLTGNQG EIRKQCNFVN SKSAELGLIN VASADSSEEG MVSSM   355

W--> 864   (ii) MOLECULE TYPE: PRT

E--> 879 FRAAMIEMGN IGVLIGTKGE IRKQCNEVNF VNSNSAELDL ATIASIVESL EDGIASVI   358

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 417

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: Linear

W- > 890   (ii) MOLECULE TYPE: PRT

E--> 906 GNIGVLTGTK GEIRKQCNFV NSNSAELDLA TIASIVESLE DGIASVI   347

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

W--> 917   (ii) MOLECULE TYPE: PRT

file: C: CRF3 Outhold VsrH939905A.htm

RAW SEQUENCE LISTING   US/08/939,905A

                    A: Sequence Listing.txt
                    H: CRF3\02092001\H939905A.raw

E--> 932 VASMIKMGNI GVLTGSQGEI RIQGNAVREN SSGLAIVVIK ESSEDGMASS F   351

file: C: CRF3 Outhold V'srH939905A.htm

VERIFICATION SUMMARY
US/08/939,905A

A:\Sequence Listing.txt
N:\CRF3\02092001\H939905A.raw

2901

VERIFICATION SUMMARY

US/08/939,905A

Input file: A:\Sequence Listing.txt

N:\CRF3\02092001\H939905A.raw

file: C: CRF3 Outhold VsrH939905A.htm